



SEQUENCE LISTING

<110> Wyeth
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Bouxsein, Mary

<120> ActRIIB Fusion polypeptides and Uses Therefor

<130> 08702.0093-00000

<140> 10/689,677

<150> October 22, 2003

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 512

<212> PRT

<213> Human

<400> 1

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Ala Gly Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu Cys Ile Tyr Tyr
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Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser Gly Leu Glu Arg
35 40 45

Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr Ala Ser Trp Ala
50 55 60

Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly Cys Trp Leu Asp
65 70 75 80

Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala Thr Glu Glu Asn
85 90 95

Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe Cys Asn Glu Arg
100 105 110

Phe Thr His Leu Pro Glu Ala Gly Gly Pro Glu Val Thr Tyr Glu Pro
115 120 125

Pro Pro Thr Ala Pro Thr Leu Leu Thr Val Leu Ala Tyr Ser Leu Leu
130 135 140

Pro Ile Gly Gly Leu Ser Leu Ile Val Leu Leu Ala Phe Trp Met Tyr
145 150 155 160

Arg His Arg Lys Pro Pro Tyr Gly His Val Asp Ile His Glu Asp Pro
165 170 175

Gly	Pro	Pro	Pro	Pro	Ser	Pro	Leu	Val	Gly	Leu	Lys	Pro	Leu	Gln	Leu				
			180					185					190						
Leu	Glu	Ile	Lys	Ala	Arg	Gly	Arg	Phe	Gly	Cys	Val	Trp	Lys	Ala	Gln				
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Leu	Met	Asn	Asp	Phe	Val	Ala	Val	Lys	Ile	Phe	Pro	Leu	Gln	Asp	Lys				
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Gln	Ser	Trp	Gln	Ser	Glu	Arg	Glu	Ile	Phe	Ser	Thr	Pro	Gly	Met	Lys				
225					230					235					240				
His	Glu	Asn	Leu	Leu	Gln	Phe	Ile	Ala	Ala	Glu	Lys	Arg	Gly	Ser	Asn				
			245						250					255					
Leu	Glu	Val	Glu	Leu	Trp	Leu	Ile	Thr	Ala	Phe	His	Asp	Lys	Gly	Ser				
			260					265					270						
Leu	Thr	Asp	Tyr	Leu	Lys	Gly	Asn	Ile	Ile	Thr	Trp	Asn	Glu	Leu	Cys				
		275					280					285							
His	Val	Ala	Glu	Thr	Met	Ser	Arg	Gly	Leu	Ser	Tyr	Leu	His	Glu	Asp				
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Val	Pro	Trp	Cys	Arg	Gly	Glu	Gly	His	Lys	Pro	Ser	Ile	Ala	His	Arg				
305					310					315					320				
Asp	Phe	Lys	Ser	Lys	Asn	Val	Leu	Leu	Lys	Ser	Asp	Leu	Thr	Ala	Val				
				325					330					335					
Leu	Ala	Asp	Phe	Gly	Leu	Ala	Val	Arg	Phe	Glu	Pro	Gly	Lys	Pro	Pro				
			340					345					350						
Gly	Asp	Thr	His	Gly	Gln	Val	Gly	Thr	Arg	Arg	Tyr	Met	Ala	Pro	Glu				
		355					360					365							
Val	Leu	Glu	Gly	Ala	Ile	Asn	Phe	Gln	Arg	Asp	Ala	Phe	Leu	Arg	Ile				
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Asp	Met	Tyr	Ala	Met	Gly	Leu	Val	Leu	Trp	Glu	Leu	Val	Ser	Arg	Cys				
385					390					395					400				
Lys	Ala	Ala	Asp	Gly	Pro	Val	Asp	Glu	Tyr	Met	Leu	Pro	Phe	Glu	Glu				
				405					410					415					
Glu	Ile	Gly	Gln	His	Pro	Ser	Leu	Glu	Glu	Leu	Gln	Glu	Val	Val	Val				
			420					425					430						
His	Lys	Lys	Met	Arg	Pro	Thr	Ile	Lys	Asp	His	Trp	Leu	Lys	His	Pro				
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Gly	Leu	Ala	Gln	Leu	Cys	Val	Thr	Ile	Glu	Glu	Cys	Trp	Asp	His	Asp				
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Ala	Glu	Ala	Arg	Leu	Ser	Ala	Gly	Cys	Val	Glu	Glu	Arg	Val	Ser	Leu				
465					470					475					480				

Ile Arg Arg Ser Val Asn Gly Thr Thr Ser Asp Cys Leu Val Ser Leu
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<213> Human

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Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
20 25 30

Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
35 40 45

Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
50 55 60

Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Val Ile Arg Gln Leu
65 70 75 80

Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
85 90 95

Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
100 105 110

Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu
115 120 125

Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
130 135 140

Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
145 150 155 160

Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
165 170 175

Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
180 185 190

Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
195 200 205

Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
210 215 220

Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
225 230 235 240

Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
245 250 255
Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
260 265 270
Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
275 280 285
Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
290 295 300
Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
305 310 315 320
Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
325 330 335
Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
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<213> Artificial Sequence
<223> Chimera/Fusion
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20 25 30
Cys Ile Tyr Tyr Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser
35 40 45
Gly Leu Glu Arg Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr
50 55 60
Ala Ser Trp Arg Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly
65 70 75 80
Cys Trp Leu Asp Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala
85 90 95
Thr Glu Glu Asn Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe
100 105 110
Cys Asn Glu Arg Phe Thr His Leu Pro Glu Ala Gly Gly Pro Glu Val

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ctgcactgct	acgcctcctg	gcgcaacagc	tctggcacca	tcgagctcgt	gaagaagggc	240
tgctggctag	atgacttcaa	ctgctacgat	aggcaggagt	gtgtggccac	tgaggagaa	300
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ccagcacctg	aactcctggg	gggaccgtca	gtcttcctct	tcccccaaaa	acccaaggac	540
acctcatga	tctcccgga	ccctgaggtc	acatgcgtgg	tgggtggacgt	gagccacgaa	600
gaccctgagg	tcaagttcaa	ctggtacgtg	gacggcgtgg	aggtgcataa	tgccaagaca	660
aagccgcggg	aggagcagta	caacagcacg	taccgtgtgg	tcagcgtcct	caccgtcctg	720
caccaggact	ggctgaatgg	caaggagtac	aagtgcgaag	tctccaacaa	agccctccca	780
gtccccatcg	agaaaaccat	ctccaaagcc	aaagggcagc	cccgagaacc	acagggtgtac	840
acctgcccc	catcccgga	ggagatgacc	aagaaccagg	tcagcctgac	ctgcctggtc	900
aaaggcttct	atcccagcga	catcgccgtg	gagtgggaga	gcaatgggca	gccggagaa	960
aactacaaga	ccacgcctcc	cgtgctggac	tccgacggct	ccttcttcct	ctatagcaag	1020
ctcaccgtgg	acaagagcag	gtggcagcag	gggaacgtct	tctcatgctc	cgtgatgcat	1080
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 <223> Linking Sequence, Gly-Ser repeat

<400> 5

Gly Ser Gly Ser
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<210> 6
 <211> 4
 <212> PRT
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<400> 6

Asp Asp Asp Lys
1